



## The phylogenetic position of *Chalcides ocellatus* (Squamata: Scincidae) from Yemen and Somalia

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### Abstract

The skink *Chalcides ocellatus* (Forsk.) is distributed around the Mediterranean region, Arabian Peninsula, and Horn of Africa. We examined *C. ocellatus* from Yemen and Somalia to clarify the biogeography of the species in the region of the Red Sea/Gulf of Aden. We examined 3612 bp of partial and complete mtDNA fragments (12S, 16S, ND1, cyt *b*, ND4, and adjacent tRNA) and 5380 bp of partial nuclear DNA fragments (BDNF, C-MOS, Rag1, PNN, and R35). Bayesian inference and Maximum-likelihood analysis placed the Somalia and Yemen specimens with those from the Eastern Mediterranean. We were unable to resolve a split between East African (Somalia) and Arabian (Yemen) populations with mtDNA, nuclear loci, and combined loci analyses.

### Introduction

*Chalcides ocellatus* is a small generalist skink found in the Mediterranean region, the Arabian Peninsula, and East Africa. The East African population from Somalia is interesting because it is disjunct, separated from the nearest *C. ocellatus* population to the west by the Ethiopian Highlands where two other species of *Chalcides* occur (Greenbaum *et al.*, 2006). The nearest population is found to the north in Yemen across the Gulf of Aden. The disjunct population in Somalia was once described as *C. o. sacchii* (Lanza) but morphological examination of specimens by Greenbaum *et al.* (2006) throughout North Africa, the Arabian Peninsula, and East Africa failed to find any valid characters to separate the Somali population from those in Arabia or further to the west. The possibility was raised that the Somali population may be relictual and that molecular evidence may show it as genetically distinct.

The *Chalcides ocellatus* complex in Carranza *et al.* (2008) displays structure and deeper divergences. Based on mtDNA, Carranza *et al.* (2008) proposed a Moroccan origin for the *C. ocellatus* complex, identified major clades, and dated divergence times among them. However, sampling from the eastern part of the range of the *C. ocellatus* complex was lacking. Kornilios *et al.* (2010) increased the range sampled to include most of the Mediterranean region and further defined the boundaries of the eastern Mediterranean clade of the *C. ocellatus* complex. One of the conclusions of Kornilios *et al.* (2010) was that the morphological similarity in the Eastern Mediterranean was mirrored by extreme genetic similarity. Human mediated dispersal was proposed as the mechanism. The Greenbaum *et al.* (2006) study did not have access to specimens from Yemen, and the Carranza *et al.* (2008) and Kornilios *et al.* (2010) studies did not include specimens from Yemen or the disjunct population in Somalia.

This study adds molecular genetic data from localities on opposite sides of the Red Sea; a Yemen locality north and east of the Strait of Bab el Mandab and the disjunct Somalia locality to south and east of the Strait of Bab el Mandab (Figure 1). Based on the phylogenetic patterns found in other studies of the region (Amer and Kumazawa, 2005; Arnold *et al.*, 2009; Pook *et al.*, 2009; Winney *et al.*, 2004; Macey *et al.*, 2008) as well as the range of *C. ocellatus* (Greenbaum *et al.*, 2006) the specimens from the Arabian Peninsula and Horn of Africa could show a genetic split across the Red Sea/Gulf of Aden. The goal of this study is to examine the phylogenetic positions of the Yemen and Somalia populations in relation to the *C. ocellatus* complex as a whole and to understand the biogeography of the *C. ocellatus* complex in the Red Sea region.